



SEQUENCE LISTING

<110> Ota, Toshio
Isogai, Takao
Nishikawa, Tetsuo
Hayashi, Koji
Otsuka, Kaoru
Yamamoto, Jun-ichi
Ishii, Shizuko
Sugiyama, Tomoyasu
Wakamatsu, Ai
Nagai, Keiichi
Otsuki, Tetsuji
Funahashi, Shin-ichi
Miyata, Shoji

<120> NOVEL GENES ASSOCIATED WITH THE
MAINTENANCE OF DIFFERENTIATION OF SMOOTH MUSCLE CELLS

<130> 06501-097001

<140> US 10/058,518

<141> 2002-01-28

<150> PCT/JP00/05059

<151> 2000-07-28

<150> US 60/183,322

<151> 2000-02-17

<150> US 60/159,590

<151> 1999-10-18

<150> JP 11-248036

<151> 1999-07-29

<150> JP 2000-118776

<151> 2000-01-11

<150> JP 2000-183767

<151> 2000-05-02

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2256

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125)...(1366)

<400> 1

A1

cagtgcgcag gcgtgagcgg tcgggccccg acgcgcgcgg gtctcgtttg gagcgggagt 60
 gagttcctga gcgagtgac ccggcagcgg gcgatagggg ggccaggtgc ctccacagtc 120
 agcc atg gca gcg ctg cgc tac gcg ggg ctg gac gac acg gac agt gag 169
 Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu
 1 5 10 15

 gac gag ctg cct ccg ggc tgg gag gag aga acc acc aag gac ggc tgg 217
 Asp Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp
 20 25 30

 gtt tac tac gcc aat cac acc gag gag aag act cag tgg gaa cat cca 265
 Val Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro
 35 40 45

 aaa act gga aaa aga aaa cga gtg gca gga gat ttg cca tac gga tgg 313
 Lys Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp
 50 55 60

 gaa caa gaa act gat gag aac gga caa gtg ttt ttt gtt gac cat ata 361
 Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile
 65 70 75

 A1 aat aaa aga acc acc tac ttg gac cca aga ctg gcg ttt act gtg gat 409
 Asn Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp
 80 85 90 95

 gat aat ccg acc aag cca acc acc cgg caa aga tac gac ggc agc acc 457
 Asp Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr
 100 105 110

 act gcc atg gaa att ctc cag ggc ccg gat ttc act ggc aaa gtg gtt 505
 Thr Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val
 115 120 125

 gtg gtc act gga gct aat tca gga ata ggg ttc gaa acc gcc aag tct 553
 Val Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser
 130 135 140

 ttt gcc ctc cat ggt gca cat gtg atc ttg gcc tgc agg aac atg gca 601
 Phe Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala
 145 150 155

 agg gcg agt gaa gca gtg tca cgc att tta gaa gaa tgg cat aaa gcc 649
 Arg Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala
 160 165 170 175

 aag gta gaa gca atg acc ctg gac ctc gct ctg ctc cgt agc gtg cag 697
 Lys Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln
 180 185 190

 cat ttt gct gaa gca ttc aag gcc aag aat gtg cct ctt cat gtg ctt 745
 His Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu
 195 200 205

 gtg tgc aac gca gca act ttt gct cta ccc tgg agt ctc acc aaa gat 793
 Val Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp
 210 215 220

ggc ctg gag acc acc ttt caa gtg aat cat ctg ggg cac ttc tac ctt 841
 Gly Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu
 225 230 235
 gtc cag ctc ctc cag gat gtt ttg tgc cgc tca gct cct gcc cgt gtc 889
 Val Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val
 240 245 250 255
 att gtg gtc tcc tca gag tcc cat cga ttt aca gat att aac gac tcc 937
 Ile Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser
 260 265 270
 ttg gga aaa ctg gac ttc agt cgc ctc tct cca aca aaa aac gac tat 985
 Leu Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr
 275 280 285
 tgg gcg atg ctg gct tat aac agg tcc aag ctc tgc aac atc ctc ttc 1033
 Trp Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe
 290 295 300
 tcc aac gag ctg cac cgt cgc ctc tcc cca cgc ggg gtc acg tcg aac 1081
 Ser Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn
 305 310 315
 gca gtg cat cct gga aat atg atg tac tcc aac att cat cgc agc tgg 1129
 Ala Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp
 320 325 330 335
 tgg gtg tac aca ctg ctg ttt acc ttg gcg agg cct ttc acc aag tcc 1177
 Trp Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser
 340 345 350
 atg caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa 1225
 Met Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu
 355 360 365
 ctg gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg 1273
 Leu Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met
 370 375 380
 ccc tca cca gaa gct cag agc gaa gag acg gcc cgg acc ctg tgg gcg 1321
 Pro Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala
 385 390 395
 ctc agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc 1366
 Leu Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
 400 405 410
 taagtggagc tcagagcggg tgggcacaca cccccgcct gtgtgtgtcc cctcacgcaa 1426
 gtgccagggc tgggcccctt ccaaagtgtc ctccaacaca gatccgcaag agtaaaggaa 1486
 ataagagcag tcacaacaga gtgaaaaatc ttaagtacca atgggaagca gggaattcct 1546
 ggggtaaaagt atcacttttc tggggctggg ctaggcatag gtctctttgc tttctgggtgg 1606
 tggcctgttt gaaagtaaaa acctgcttgg tgtgtagggt ccgtatctcc ctggagaagc 1666
 accagcaatt ctctttcttt tactgttata gaatagcctg aggtccccctc gtcccatcca 1726
 gctaccacca cgccaccac tgcagccggg ggctggcctt ctctacttta gggaagaaaa 1786
 agcaagtgtt cactgctcct tgctgcattg atccaggaga taattgtttc attcatcctg 1846

A1

```

acc'aagactg agccagctta gcaactgctg gggagacaaa tctcagaacc ttgtcccagc 1906
cagtgaggat gacagtgaca cccagagggg gtagaatacg cagaactacc aggtggcaaa 1966
gtacttgtca tagactcctt tgctaattgct atgcaaaaaa ttcttttagag attataacaa 2026
atTTTTcaaa tcattcctta gataccttga aaggcaggaa gggaagcgta tataacttaag 2086
aatacacagg atatTTTggg gggcagagaa taaaacgtta gttaatccct ttgtctgtca 2146
atcacagtct cagttctctt gctttcacat tgtacttaaa cctcctgctg tgcctcgcat 2206
cctatgctta ataaaagaac atgcttgaat atcaaaaaaa aaaaaaaaac 2256

```

<210> 2

<211> 414

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu Asp
1 5 10 15
Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val
20 25 30
Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys
35 40 45
Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
50 55 60
Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
65 70 75 80
Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
85 90 95
Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
100 105 110
Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val Val
115 120 125
Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
130 135 140
Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg
145 150 155 160
Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys
165 170 175
Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His
180 185 190
Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val
195 200 205
Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly
210 215 220
Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val
225 230 235 240
Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile
245 250 255
Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu
260 265 270
Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp
275 280 285
Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser
290 295 300
Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala
305 310 315 320
Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp
325 330 335
Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met

340 345 350
 Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu
 355 360 365
 Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro
 370 375 380
 Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu
 385 390 395 400
 Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
 405 410

<210> 3
 <211> 251
 <212> DNA
 <213> Gallus gallus

<220>
 <221> CDS
 <222> (3)...(251)

<400> 3
 ag gag cgc acc acc aag gac ggc tgg gtt tac tac gcc aat cac ttg 47
 Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu
 1 5 10 15
 gaa gaa aaa aca cag tgg gaa cat cca aaa tct ggg aag agg aaa cgt 95
 Glu Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg
 20 25 30
 gtt gca gga ggt ctg cca tat gga tgg gag cag gag act gat gaa aat 143
 Val Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn
 35 40 45
 gga cag gtc tat ttt gta gac cac ata aac aaa aga act acc tat ctg 191
 Gly Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu
 50 55 60
 gat cca aga ttg gcc ttt aca gtt gaa gat aat cca gca aag cca cct 239
 Asp Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro
 65 70 75
 act aga caa aaa 251
 Thr Arg Gln Lys
 80

<210> 4
 <211> 83
 <212> PRT
 <213> Gallus gallus

<400> 4
 Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu Glu
 1 5 10 15
 Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg Val
 20 25 30
 Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly
 35 40 45

Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp
 50 55 60
 Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro Thr
 65 70 75 80
 Arg Gln Lys

<210> 5
 <211> 30
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated oligonucleotide

<400> 5
 agcaucgagu cgccuuguu ggccuacugg 30

<210> 6
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

<400> 6
 gcggctgaag acggcctatg tggccttttt tttttttttt tt 42

<210> 7
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

<400> 7
 agcatcgagt cggccttggt g 21

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

<400> 8
 gcggctgaag acggcctatg t 21

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

A1

<400> 9
gcaggaacat ggcaagggcg agtg 24

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 10
gggcaggagc tgagcggcac aaa 23

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 11
ggtggctttg ctggattatc tt 22

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 12
gttgcaaggag gtctgccata tg 22

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 13
tacggaagtg ttactttctgc 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 14

tgtgggaggt tttttctcta

20

<210> 15

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

A1 <400> 15

gttttcccag tcacgac

17

<210> 16

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 16

caggaaacag ctatgac

17
